

REMARKS

Claims 1-20 are pending in the present application, however, claims 19 and 20 have been withdrawn from consideration as non-elected. Non-elected claims 19 and 20 are canceled herein, the restriction requirement having been made final. Applicants reserve the right to prosecute the subject matter of these claims in a divisional application.

In the pending Office Action, the Examiner has indicated that claims 5-6 are allowable and claims 9-18, while not rejected, are objected to on the grounds of either improper dependent form or because they are dependent on a rejected claim. Claims 1-4, 7 and 8 stand rejected.

Claims 1-4 and 7-8 are rejected under 35 U.S.C. § 112, first paragraph, on the grounds that the specification, while containing enabling support for isolated polynucleotides as set forth in SEQ ID NOS:1 and 2 does not enable the rejected claims in their full scope. This rejection appears to be based on the Office's reading of the claims to include the entire chromosome on which these sequences are located. Applicants respectfully submit that the claims of this invention are not intended to claim an entire chicken chromosome. Claims 1-4 are limited to sequences that contain at least a portion 17 nucleotides long from the specifically recited sequences of SEQ ID NO:1 or SEQ ID NO:2 and which are 17 to about 1000 nucleotides long. Such probes cannot span an entire chromosome since the maximum length of the claimed probe is about 1000 nucleotides. The claims are intended to read on probes the binding sequences of which overlap with the preferred probes of SEQ ID NOS:1 and 2 and include sequences adjacent to SEQ ID NOS:1 and 2 along the gene of origin. There is absolutely no unpredictability whatsoever as to the precise identity of these

adjacent sequences which abut SEQ ID NOS:1 and 2 in the chicken. See SEQ ID NOS:5 and 6 and references cited in the Information Disclosure Statement of record in this application.

It is apparent that the language of claims 1 and 3 has resulted in a misunderstanding as to the intended claim scope. Therefore, Applicants have amended the claims herein to improve the readability of the claims. The claims now recite a probe which consists essentially of 17 to about 1000 consecutive nucleotides of the chicken Rfp-Y or B Class I genes. Claims 21-26 have been added to specifically claim certain embodiments which were covered by claim 1 prior to amendment. For support of the claim amendments, the Office may refer to paragraphs 62-64, which discuss probes having longer sequences encompassing adjacent regions of the gene of origin and homologous probes. In view of these amendments and the discussion above, Applicants request withdrawal of the rejection of claims 1-4 as not enabled.

Claims 7 and 8 also are rejected on the grounds that the specification does not provide enabling support. These claims are dependent on claims 5 and 6, which are considered enabled by the Office, and are directed to a fragment of a probe, the complete sequence of which is provided in the present specification. These claims have been amended herein in independent form. The scope of the amended claims is the same. Applicants respectively submit that a person of skill in the art, described in the pending Office Action as a person having a Ph.D. degree and laboratory experience, would have no trouble whatsoever creating any desired fragment of a probe when the complete sequence of the probe has been provided. It would be a matter of mere routine for any skilled technician to create any fragment of this fully disclosed probe using the guidelines provided (that the fragment is to be 17 to 625 (or 674) nucleotides long).

There can be no question that each and every probe encompassed by claims 7-8 is fully described and enabled by the specification and that no guesswork or unpredictability could be involved in cutting the probes of SEQ ID NOS:1 or 2 at any desired location. Applicants therefore request that the rejection of claims 7-8 under 35 U.S.C. § 112, first paragraph be withdrawn.

Claims 1-4 and 11 are rejected under 35 U.S.C. § 102(b) as anticipated by Shiina et al. Shiina et al. disclose the quail TAP2 gene and do not teach a probe as claimed in this application, or indeed any probes. The Office points to an internal segment of the much larger quail gene, seventeen nucleotide bases long, which has 100% homology to a portion of SEQ ID NO:1 of the present invention. This quail gene does not meet all the limitations of the amended claims here rejected, for example, a probe of 17 to about 1000 consecutive nucleotides of the chicken Class I gene. Moreover, there is nothing in the reference that would motivate a skilled person to excise this seventeen base section (to which no special attention has been called by Shiina et al.), absent hindsight, for use as a probe or for any reason at all. Certainly, there is no motivation to extend this sequence to include more 3' or 5' regions of the chicken genome as is taught here since those sequences are not provided by Shiina et al.

The Office also points out a portion of the quail gene sequences which shows homology to nucleotides 1-665 of SEQ ID NO:2 of this invention, a sequence disclosed as having 675 nucleotide bases. Shiina et al. cannot anticipate any claim unless it teaches each and every limitation of that claim. The Shiina et al. quail gene does not anticipate the probes of claims 1-2, which do not relate to SEQ ID NO:1. The gene does not anticipate the probes of claims 3-4 because the reference does not teach any probe, or any sequence having 17 to about 1000 consecutive nucleotides of the

chicken Rfp-Y or B Class I genes, and does not disclose any sequence having about 17 consecutive nucleotide of SEQ ID NO:2. The reference does not anticipate new claims 22 or 24 because it does not teach a probe consisting essentially of a sequence homologous to 17 to about 1000 consecutive nucleotides of Chicken Class I genes. Applicants therefore request that the Office withdraw the rejection of claims 1-4 and 11 as anticipated by Shiina et al.

Claims 3-4 are rejected under 35 U.S.C. § 102(e) as anticipated by Bacon et al. Like Shiina et al., Bacon et al. disclose a gene. Although a portion of that gene is homologous to a portion of SEQ ID NO:2, the gene of Bacon et al. does not anticipate claims 3-4 of this application because it does not meet each and every claim limitation. The discussion above with regard to SEQ ID NO: 1 and Shiina et al. are applicable here, therefore applicants refer the Office to the discussion above. In summary, Bacon et al. do not teach a probe and do not disclose a sequence of 17-1000 nucleotides in length.

Applicants also submit that there is no motivation to excise the portion of the Bacon et al. gene identified as homologous to a portion of SEQ ID NO:2 from the complete sequence for use as a probe or for any reason whatsoever. Therefore, Bacon et al. cannot provide a basis to reject the claims of this invention. Applicants request that the Office withdraw the rejection of claims 3-4 over Bacon et al.

Claims 3-4 and 11 are rejected under 35 U.S.C. § 102(b) as anticipated by Chaussé et al. Like Shiina et al. and Bacon et al., this reference does not disclose a probe. It discloses a gene, a portion of which shows homology to some of the embodiments described in this application. The sequence of Chaussé et al. does not meet the limitations of claims 3 or 4 as amended or of new

claims 21-24. For example, this reference does not disclose a probe of 17 to about 1000 nucleotides in length or any probe, and provides no motivation to excise the probes of this invention from the complete gene. The gene of Chaussé et al., like those disclosed in the other references cited here, contains large sequences which do not meet the limitations of the rejected claims. Applicants request that the rejection of claims 3-4 and 11 be withdrawn.

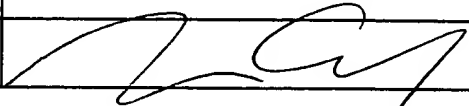
Claims 7-12 and 14 are objected to under 37 C.F.R. § 1.75(c) as being of improper dependent form for failing to further limit the subject matter of a previous claim. Claim 7 is dependent on claim 5, which recites "The probe of SEQ ID NO:1." The probe of SEQ ID NO:1 consists of a sequence of 626 nucleotides. Claim 7 has been amended and now recites a fragment of this probe having 17 to 625 nucleotides and therefore limits the previous claim by one or more nucleotides. Claim 8 also has been amended in the same manner to delete the term "about." Applicants submit that these amendments correct the improper dependency of these claims.

Claims 9 and 11 have been canceled herein. Claims 10 and 12 have been rewritten in independent form as suggested in the Office Action. Applicants therefore submit that the form of these claims is correct.

Claims 13 and 15-18 are objected to on the grounds that they are dependent upon rejected independent claims 1 and 3. Applicants respectfully submit that independent claims 1 and 3 are allowable in view of the amendments herein and the discussions above, and request that the objections to these claims on this basis be withdrawn.

Applicants submit that the application is in condition for allowance and request that the Office reconsider the amended claims.

U.S. Application Serial No. 09/870,521
Filed: June 1, 2001

RESPECTFULLY SUBMITTED,					
NAME AND REG. NUMBER	Martha Cassidy, Registration No.: 44,066				
SIGNATURE				DATE	4/8/03
ADDRESS	Rothwell, Figg, Ernst & Manbeck Suite 800, 1425 K Street, N.W.				
CITY	Washington	STATE	D.C.	ZIP CODE	20005
COUNTRY	U.S.A.	TELEPHONE	202-783-6040	FAX	202-783-6031

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